

09821.160

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=> s translat###(10a)identif#####(10a)(polypeptide or protein#)(10a)(on or within)(10a)cell#

L1 0 TRANSLAT###(10A) IDENTIF#####(10A) (POLYPEPTIDE OR PROTEIN#) (10A) (ON OR WITHIN) (10A) CELL#

=> s identif#####(10a)protein#(10A)(on or within)(10a)cell#

L2 419 IDENTIF#####(10A) PROTEIN#(10A) (ON OR WITHIN) (10A) CELL#

=> s l2 and (translat###(10a)trancri#####)

L3 0 L2 AND (TRANSLAT###(10A) TRANCRI#####)

=> s l2 and (translat###(10a)transcri#####)

L4 0 L2 AND (TRANSLAT###(10A) TRANSCRI#####)

=> s l2 and polymerase chain reaction#

L5 17 L2 AND POLYMERASE CHAIN REACTION#

=> s l5 and translat### and trancri#####

L6 0 L5 AND TRANSLAT### AND TRANCRI#####

=> s l2 and translat### and transcri#####

L7 10 L2 AND TRANSLAT### AND TRANSCRI#####

=> s l7 and polymerase chain reaction#

L8 1 L7 AND POLYMERASE CHAIN REACTION#

=> d l8 bib ab kwic

L8 ANSWER 1 OF 1 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 2001:151519 BIOSIS

DN PREV200100151519

TI Gene function analysis by amber stop codon suppression: CMBF is a nuclear protein that supports growth and development of Dictyostelium amoebae.

AU Winckler, Thomas [Reprint author]; Trautwein, Christine; Tschepke, Christina; Neuhaeuser, Christin; Zuendorf, Ilse; Beck, Peter; Vogel, Guenter; Dinger mann, Theodor

CS Biozentrum, Institut fuer Pharmazeutische Biologie, Universitaet Frankfurt/M., D-60439, Frankfurt am Main, Germany
winckler@em.uni-frankfurt.de

SO Journal of Molecular Biology, (26 January, 2001) Vol. 305, No. 4, pp. 703-714. print.

CODEN: JMOBAK. ISSN: 0022-2836.

DT Article

LA English

ED Entered STN: 28 Mar 2001

Last Updated on STN: 15 Feb 2002

AB The C-module-binding factor, CMBF, is a nuclear DNA-binding **protein** which was originally **identified** through its specific binding to a promoter element **within** the retrotransposable element TRE5-A of Dictyostelium discoideum AX2 **cells**. In order to analyse putative physiological functions of CMBF for the TRE5-A-hosting D. discoideum cells, we used a novel strategy to create mutant cell lines which stably underexpressed functional CMBF. An amber (UAG) **translation** stop codon was introduced into the chromosomal copy of the CMBF-encoding gene (cbfA), and an amber suppressor tRNA gene was expressed in the same mutant cells. Due to the low efficiency of **translation** stop codon suppression in this system all recovered cell lines expressed <20% of wild-type CMBF levels. The mutant cell lines displayed strong growth phenotypes when plated on their natural food source, bacteria. We show evidence that growth reduction was due to impaired phagocytosis of bacteria in the mutants. All obtained mutants showed a strong developmental defect which was defined by the formation of very small fruiting bodies. The strength of the developmental phenotype appeared to depend upon the residual CMBF levels maintained in the mutants. We propose that CMBF is a general **transcription** regulator which supports the normal expression of several genes required for the maintenance of high proliferation rates of D. discoideum amoebae as well as proper aggregation and development. Our results demonstrate that amber stop codon suppression may be a useful strategy to stably underexpress proteins whose coding genes cannot be successfully disrupted by homologous recombination.

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IT Methods & Equipment

PCR [**polymerase chain reaction**]: DNA amplification, amplification method, in-situ recombinant gene expression detection, sequencing techniques; electrophoretic mobility shift assay: gene mapping method, restriction fragment. . .

=> s 12 and PCR

L9 12 L2 AND PCR

=> s 19 and translat### and transcript###

L10 1 L9 AND TRANSLAT### AND TRANSCRIPT###

=> d l10 bib ab

L10 ANSWER 1 OF 1 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 2001:151519 BIOSIS

DN PREV200100151519

TI Gene function analysis by amber stop codon suppression: CMBF is a nuclear protein that supports growth and development of Dictyostelium amoebae.

AU Winckler, Thomas [Reprint author]; Trautwein, Christine; Tschepke,

Christina; Neuhaeuser, Christin; Zuendorf, Ilse; Beck, Peter; Vogel, Guenter; Dingermann, Theodor

CS Biozentrum, Institut fuer Pharmazeutische Biologie, Universitaet Frankfurt/M., D-60439, Frankfurt am Main, Germany
winckler@em.uni-frankfurt.de

SO Journal of Molecular Biology, (26 January, 2001) Vol. 305, No. 4, pp. 703-714. print.
CODEN: JMOBAK. ISSN: 0022-2836.

DT Article

LA English

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Last Updated on STN: 15 Feb 2002

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09/821.160

=> s (identif##### or detect###) (10a) (polypeptide# or protein#) (10a) (contact###
cell##### membrane# or on cell# or within cell#)

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L1 62424 (IDENTIF##### OR DETECT###) (10A) (POLYPEPTIDE# OR PROTEIN#) (10A)
(CONTACT### CELL##### MEMBRANE# OR ON CELL# OR WITHIN CELL#)

=> s l1 and (translat###(10a)transcri#####)

L2 586 L1 AND (TRANSLAT###(10A) TRANSCRI#####)

=> s (identif##### or detect###) (5A) (polypeptide# or protein#) (5a) (contact### or
bind###) (5a) (cell##### membrane or on cell# or within cell#)

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CONTACT### OR BIND###) (5A) (CELL##### MEMBRANE OR ON CELL# OR
WITHIN CELL#)

=> s l3 and (translat###(5A)transcri#####)

L4 18 L3 AND (TRANSLAT###(5A) TRANSCRI#####)

=> dup rem l4

PROCESSING COMPLETED FOR L4

L5 8 DUP REM L4 (10 DUPLICATES REMOVED)

=> d l5 1-8 bib ab kwic

L5 ANSWER 1 OF 8 MEDLINE on STN DUPLICATE 1

AN 2002147235 MEDLINE

DN 21874805 PubMed ID: 11878877

TI Analysis of early region 1 of porcine adenovirus type 3.

AU Zhou Y; Tikoo S K

CS Virology Group, University of Saskatchewan, Saskatoon, Saskatchewan, S7N
5E3, Canada.

SO VIROLOGY, (2001 Dec 5) 291 (1) 68-76.

Journal code: 0110674. ISSN: 0042-6822.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 200204

ED Entered STN: 20020308

Last Updated on STN: 20020403

Entered Medline: 20020401

AB To identify the proteins encoded by the porcine adenovirus 3 (PAV-3) E1
region, rabbit antisera were prepared using a bacterial fusion protein
encoding E1A, E1B(small), or E1B(large) protein. Sera against E1A,
E1B(small), and E1B(large) immunoprecipitated a protein of 35, 23, and 53
kDa, respectively, in in vitro **translated** and
transcribed mRNA and PAV-3 infected cells. To determine the role
of E1 proteins in PAV-3 replication, we constructed vectors with a
deletion(s) in the E1 region. Mutant PAV211, containing deletions in E1A
and E3, grew to titers similar to wild-type in VIDO R1 cells (E1A
complementing) but not in swine testicular (ST) cells. No early protein
(E1B(small), DNA **binding protein**) expression could be
detected in PAV211 infected ST cells by Western blots.
Mutant PAV212, containing deletions in E1B(small) and E3, grew to
wild-type titers in VIDO R1 or ST cells. These deletions were
successfully rescued, resulting in recombinant PAV214, containing
deletions in E1A, E1B(small), and E3. However, mutant PAV-3, containing a
triple stop codon inserted in the E1B(large) coding sequence, could not be
isolated. Next, we constructed a recombinant PAV216 by inserting the
green fluorescent protein gene flanked by a promoter and a poly(A) in the
E1A region of the PAV214 genome. Both PAV214 and PAV216 replicate as

efficiently as wild-type in VIDO R1 cells. These results suggested that (a) E1A is essential for virus replication and is required for the activation of other PAV-3 early genes, (b) E1B(small) is not essential for replication of PAV-3, and (c) E1B(large) is essential for virus replication. Moreover, the PAV216 vector can be used for the expression of a transgene.

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AB . . . protein. Sera against E1A, E1B(small), and E1B(large) immunoprecipitated a protein of 35, 23, and 53 kDa, respectively, in in vitro **translated** and **transcribed** mRNA and PAV-3 infected cells. To determine the role of E1 proteins in PAV-3 replication, we constructed vectors with a . . . to wild-type in VIDO R1 cells (E1A complementing) but not in swine testicular (ST) cells. No early protein (E1B(small), **DNA binding protein**) expression could be **detected** in PAV211 infected ST **cells** by Western blots. Mutant PAV212, containing deletions in E1B(small) and E3, grew to wild-type titers in VIDO R1 or ST. . .

L5 ANSWER 2 OF 8 MEDLINE on STN DUPLICATE 2
AN 96336514 MEDLINE
DN 96336514 PubMed ID: 8738726
TI Primary cultured normal human hepatocytes for hepatitis B virus receptor studies.
AU Mabit H; Vons C; Dubanchet S; Capel F; Franco D; Petit M A
CS Institut National de la Sante de la Recherche Medicale Unite, Unite, Clamart, France.
SO JOURNAL OF HEPATOLOGY, (1996 Apr) 24 (4) 403-12.
Journal code: 8503886. ISSN: 0168-8278.
CY Denmark
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199612
ED Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961211
AB BACKGROUND/AIMS: We analyzed the hepatitis B virus envelope specificities (HBs, preS2 and preS1) involved in virus attachment to normal human hepatocytes, and we performed in vitro hepatitis B virus infection experiments without addition of dimethyl sulfoxide and polyethylene glycol, which may affect cell membrane integrity, in order to study further the early steps of the life cycle of the hepatitis B virus. METHODS: Primary normal human hepatocytes were prepared from surgical biopsies by the two-step collagenase perfusion technique, and cultured in a fetal calf serum-free medium supplemented with 10(-6) M dexamethasone. Cell-binding assays, ligand blotting and immunohistochemistry experiments were carried out using our anti-idiotypic (Ab2) antibodies (Ab2s/preS1, Ab2s/preS2 and Ab2s/HBs). RESULTS: Probing primary normal human hepatocytes, the 35-kDa major preS1-**binding protein** (preS1-BP35) we have previously **identified** in human hepatoma HepG2 **cells** was recognized in blotting, whereas both HBs- and preS1-specificities of the hepatitis B virus envelope interacted strongly with normal human hepatocyte cell membrane in cell-binding assays and immunohistochemistry experiments. Hepatitis B virus infectivity studies confirmed a great inter-experimental variability depending on donors and liver perfusion, and demonstrated a great intra-experimental variability depending on the serum-derived hepatitis B virus isolate used for the inoculation. In our culture conditions, only increased detection of the RC and CCC DNA forms of hepatitis B virus in cells and of hepatitis B virus surface antigens in medium was observed 4 to 8 days after exposure of cells to hepatitis B virus. CONCLUSION: These findings support a potential role for preS1-BP35 as a receptor protein for hepatitis B virus. In our hands, limitation(s) in the hepatitis B virus life cycle may occur at some step after virion binding, and likely result from complex

regulation of reverse **transcription** of the RNA and **translation** of core protein by extrahepatic host factors or/and by the virus itself. However, the normal human hepatocyte model developed here is available for studying the initial steps in hepatitis B virus entry into cells.

AB . . . carried out using our anti-idiotypic (Ab2) antibodies (Ab2s/preS1, Ab2s/preS2 and Ab2s/HBs). RESULTS: Probing primary normal human hepatocytes, the 35-kDa major preS1-binding **protein** (preS1-BP35) we have previously **identified** in human hepatoma HepG2 **cells** was recognized in blotting, whereas both HBs- and preS1-specificities of the hepatitis B virus envelope interacted strongly with normal human. . . B virus life cycle may occur at some step after virion binding, and likely result from complex regulation of reverse **transcription** of the RNA and **translation** of core protein by extrahepatic host factors or/and by the virus itself. However, the normal human hepatocyte model developed here. . .

L5 ANSWER 3 OF 8 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

AN 97183353 EMBASE

DN 1997183353

TI Multiple myosin isozymes and hair-cell function.

AU Gillespie P.G.; Hasson T.; Garcia J.A.; Corey D.P.

CS P.G. Gillespie, Department of Physiology, Johns Hopkins University, Baltimore, MD 21205, United States

SO Cold Spring Harbor Symposia on Quantitative Biology, (1996) 61/- (309-318).

Refs: 79

ISSN: 0091-7451 CODEN: CSHSAZ

CY United States

DT Journal; Conference Article

FS 029 Clinical Biochemistry

LA English

SL English

AB The above enumeration does not conclusively summarize identities and functions of all hair-cell myosin isozymes. The RT-PCR screen described by Sole et al. (1994) demonstrated that other myosin isozymes, including myosin I α and myosin X, are also found in hair-cell-containing epithelia; in addition, primer sets used may have missed other classes; for example, homologous of myosins III and Vb. Additional cataloging of myosins mRNAs from frog sacculus and other auditory and vestibular tissues will no doubt identify additional myosin isozymes expressed in hair cells. Myosin molecules besides myosin VI and VIIa are likely to be essential for hair cells. Genes for several myosin isozymes, including those for myosins I β , I γ , and VIIb, are predicted to map closely to the chromosomal locations of at least one human deafness gene (Hasson et al. 1996). Mutations in their hair-cell myosin isozymes may not manifest as human deafnesses if the isozyme in question is employed for other essential roles. Although distribution of myosin molecules within the auditory and vestibular systems is complicated, we believe that a specific, principal role can be ascribed to each isozyme. Myosin V is not found in hair cells and likely serves the same role in afferent nerve processes that it plays elsewhere in the nervous system. Myosin I- probably mediates adaptation and may contribute to transport of proteins throughout stereocilia. Myosin VI appears to cross-link actin filaments within the cuticular plate and perhaps between the cuticular plate and stereociliary rootlets; mutations in myosin VI may disrupt these structures and prevent bundle formation. Myosin VIIa may actually hold stereocilia together, mutations in myosin VIIa may therefore cause stereocilia to splay apart, preventing proper assembly into a hair bundle. Myosin I β , VI, and VIIa are each at unusually high concentrations in bundles of the most newly formed hair cells, usually at the sensory epithelium's periphery (Gillespie et al. 1993; T. Hasson et al., in

prepare); these three isozymes may therefore play additional, more specialized roles during hair-bundle development (Tilney et al. 1992). In the future, we expect that exciting results will come from experiments designed to test these predictions. A key conclusion from hair-cell myosin localization is that these myosin molecules are not necessarily concentrated in regions of high actin density. Despite the similarity of their catalytic domains, each of the myosin isozymes found in hair cells has a distinctive subcellular localization. Furthermore, each hair-cell myosin isozyme appears in multiple specific locations. The ability of myosin molecules to bind to and translocate along actin filaments must therefore be heavily regulated; for dictating location, the affinity of myosin molecules for other proteins may be just as important as their affinity for actin. The nonhomologous tail domains of each class must contribute substantially to this differential localization. A critical goal for the field is therefore **identification** of hair-cell proteins that bind to myosin molecules, because their localization and abundance relative to each myosin isozyme may establish the final destination of a given myosin molecule. Finally, we wonder why myosin molecules would be employed in capacities that appear, at first consideration, to be entirely structural. In particular, our hypothesized roles for myosins VI and VIIa-maintaining cuticular-plate and bundle structural integrity-do not require force-producing molecules. Proteins that simply cross-link actin or connect actin to specific membrane receptors would seem to function adequately. Because the cell expends considerable energy to **transcribe** and **translate** relatively large myosin motor domains instead of smaller actin-binding structures, it seems likely that actin-activated ATPase plays a fundamental role in the behavior of these myosin isozymes. Because myosins VI and VIIa are not simply targeted to distal ends of actin filaments, but are instead found in association with specific actin-filament domains, the role of the motor activity must be relatively subtle. It seems likely that by understanding this paradox, we will understand the precise role of each myosin isozyme in the hair cell.

AB . . . tail domains of each class must contribute substantially to this differential localization. A critical goal for the field is therefore **identification** of hair-cell proteins that bind to myosin molecules, because their localization and abundance relative to each myosin isozyme may establish the final destination of a. . . actin or connect actin to specific membrane receptors would seem to function adequately. Because the cell expends considerable energy to **transcribe** and **translate** relatively large myosin motor domains instead of smaller actin-binding structures, it seems likely that actin-activated ATPase plays a fundamental role. . .

L5 ANSWER 4 OF 8 MEDLINE on STN DUPLICATE 3
 AN 94263234 MEDLINE
 DN 94263234 PubMed ID: 8203918
 TI Overexpression of iron-responsive element-binding protein and its analytical characterization as the RNA-binding form, devoid of an iron-sulfur cluster.
 AU Basilion J P; Kennedy M C; Beinert H; Massinople C M; Klausner R D; Rouault T A
 CS National Institutes of Health, National Institute of Child Health and Human Development, Bethesda, Maryland 20892.
 NC GM 34812 (NIGMS)
 SO ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1994 Jun) 311 (2) 517-22. Journal code: 0372430. ISSN: 0003-9861.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199407
 ED Entered STN: 19940714
 Last Updated on STN: 19970203

Entered Medline: 19940701

AB The iron-responsive element-binding protein (IRE-BP) has been defined and **identified** as an **RNA-binding protein** found in iron-deprived eukaryotic **cells**. IRE-BP binds to stem-loop structures, iron-responsive elements (IRES), which are located in the untranslated regions of the mRNAs for several genes including ferritin, and the transferrin receptor. When bound, IRE-BP prevents ferritin **translation** and stabilizes the transferrin receptor **transcript**. When cells are iron replete, an iron-sulfur cluster is ligated to the IRE-BP, the protein loses RNA binding properties, and it acquires aconitase activity. Cytosolic aconitase from liver can be converted into the IRE-BP by oxidative removal of its Fe-S cluster. We describe here overexpression of IRE-BP in baculovirus-infected insect cells which yields IRE-BP devoid of an iron-sulfur cluster. We describe a one-step purification of the IRE-BP and a quantitative analysis of Fe, S₂⁻, S₀, protein, and enzyme activity on IRE-BP, as obtained in cell lysates, after purification, and after reconstitution to active aconitase. On the average not more than 3% of the over-expressed purified protein contained an intact Fe-S cluster, and it was demonstrated that that cluster was not lost during purification. Scatchard analysis of RNA-binding data was compatible with a single high-affinity RNA-binding form of the IRE-BP. Active aconitase could be reconstituted from the purified IRE-BP obtained from the expression system by addition of iron, thiol, and sulfide, and the characteristic epr spectrum of the 3Fe form of cytosolic aconitase was obtained after ferricyanide oxidation of the reconstituted material.

AB The iron-responsive element-binding protein (IRE-BP) has been defined and **identified** as an **RNA-binding protein** found in iron-deprived eukaryotic **cells**. IRE-BP binds to stem-loop structures, iron-responsive elements (IRES), which are located in the untranslated regions of the mRNAs for several genes including ferritin, and the transferrin receptor. When bound, IRE-BP prevents ferritin **translation** and stabilizes the transferrin receptor **transcript**. When cells are iron replete, an iron-sulfur cluster is ligated to the IRE-BP, the protein loses RNA binding properties, and.

L5 ANSWER 5 OF 8 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
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AN 93040298 EMBASE

DN 1993040298

TI An essential yeast gene encoding a TTAGGG repeat-binding protein.

AU Brigati C.; Kurtz S.; Balderes D.; Vidali G.; Shore D.

CS Department of Microbiology, College of Physicians and Surgeons, Columbia University, 701 West 168th Street, New York, NY 10032, United States

SO Molecular and Cellular Biology, (1993) 13/2 (1306-1314).

ISSN: 0270-7306 CODEN: MCEBD4

CY United States

DT Journal; Article

FS 022 Human Genetics

029 Clinical Biochemistry

LA English

SL English

AB A yeast gene encoding a DNA-binding protein that recognizes the telomeric repeat sequence TTAGGG found in multicellular eukaryotes was identified by screening a λ gt11 expression library with a radiolabeled TTAGGG multimer. This gene, which we refer to as TBF1 (TTAGGG repeat-binding factor 1), encodes a polypeptide with a predicted molecular mass of 63 kDa. The TBF1 protein, produced in vitro by **transcription** and **translation** of the cloned gene, binds to (TTAGGG)(n) probes and to a yeast telomeric junction sequence that contains two copies of the sequence TTAGGG separated by 5 bp. TBF1 appears to be identical to a previously described yeast TTAGGG-repeat binding activity called TBF α . TBF1 produced in vitro yields protein-DNA complexes with

(TTAGGG)(n) probes that have mobilities on native polyacrylamide gels identical to those produced by partially purified TBF α from yeast cells. Furthermore, when extracts are prepared from a strain containing a TBF1 gene with an antigen tag, we find that the antigen copurifies with the predominant (TTAGGG)(n)-binding activity in the extracts. The DNA sequence of TBF1 was determined. The predicted protein sequence suggests that TBF1 may contain a nucleotide-binding domain, but no significant similarities to any other known **proteins** were **identified**, nor was an obvious DNA-binding motif apparent. Diploid cells heterozygous for a tbfl::URA3 insertion mutation are viable but upon sporulation give rise to tetrads with only two viable spores, both of which are Ura-, indicating that the TBF1 gene is essential for growth. Possible functions of TBF1 (TFB α) are discussed in light of these new results.

AB . . . factor 1), encodes a polypeptide with a predicted molecular mass of 63 kDa. The TBF1 protein, produced in vitro by **transcription** and **translation** of the cloned gene, binds to (TTAGGG)(n) probes and to a yeast telomeric junction sequence that contains two copies of . . . The predicted protein sequence suggests that TBF1 may contain a nucleotide-binding domain, but no significant similarities to any other known **proteins** were **identified**, nor was an obvious DNA-binding motif apparent. Diploid cells heterozygous for a tbfl::URA3 insertion mutation are viable but upon sporulation give rise to tetrads with only two viable spores, . . .

L5 ANSWER 6 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 4

AN 1989:160558 BIOSIS

DN PREV198987082659; BA87:82659

TI BIOCHEMICAL AND IMMUNOLOGICAL COMPARISONS OF CARBOHYDRATE-BINDING PROTEIN 35 AND AN IGE-BINDING PROTEIN.

AU LAING J G [Reprint author]; ROBERTSON M W; GRITZMACHER C A; WANG J L; LIU F-T

CS DIV OF MOL BIOL, MED BIOL INST, 11077 N TORREY PINES RD, LA JOLLA, CALIF 92037, USA

SO Journal of Biological Chemistry, (1989) Vol. 264, No. 4, pp. 1907-1910. CODEN: JBCHA3. ISSN: 0021-9258.

DT Article

FS BA

LA ENGLISH

ED Entered STN: 25 Mar 1989

Last Updated on STN: 25 Mar 1989

AB The predicted amino acid sequence of carbohydrate-binding protein 35 (CBP35; Mr .apprx. 35,000), a galactose-specific lectin in many mouse and human cells, has been compared to the predicted sequence of an IgE-binding protein (ϵ BP) originally **identified** in rat basophilic leukemia cells. The sequences of the two proteins showed that: (a) 85% of the amino acid residues are identical; (b) the polypeptide chains are comprised of two distinct domains; and (c) highly conserved internal repetitive sequences are present. Consistent with these observations, antisera raised against CBP35 or against a synthetic peptide derived from the ϵ BP sequence cross-reacted with both proteins. Moreover, fractionation of extracts of mouse 3T3 fibroblasts over an IgE-Sepharose affinity column showed that CBP35 bound to IgE; this binding was reversed by addition of lactose. Conversely, fractionation of extracts of rat basophilic leukemia cells over an affinity column of Sepharose derivatized with N-(ϵ -aminocaproyl)-D-galactosamine showed that ϵ BP was a galactose-binding protein. Furthermore, ϵ BP bound to IgE-Sepharose could be eluted by lactose. Finally, **transcription** and **translation** in vitro of the cDNA corresponding to ϵ BP yielded a polypeptide containing carbohydrate-binding activity. All of these results strongly support the conclusion that CBP35 and ϵ BP are mouse and rat homologues, respectively.

AB. . . .apprx. 35,000), a galactose-specific lectin in many mouse and human cells, has been compared to the predicted sequence of an IgE-binding protein (εBP) originally identified in rat basophilic leukemia cells. The sequences of the two proteins showed that: (a) 85% of the amino acid residues are identical; (b) the polypeptide. . . . with N-(ε-aminocaproyl)-D-galactosamine showed that εBP was a galactose-binding protein. Furthermore, εBP bound to IgE-Sepharose could be eluted by lactose. Finally, transcription and translation in vitro of the cDNA corresponding to εBP yielded a polypeptide containing carbohydrate-binding activity. All of these results strongly support. . . .

IT Descriptors

RAT BASOPHILIC LEUKEMIA CELL HUMAN MOUSE GALACTOSE-SPECIFIC LECTIN
MOLECULAR SEQUENCE DATA AMINO ACID SEQUENCE COMPARISON CONSERVED
SEQUENCES COMPLEMENTARY DNA TRANSCRIPTION TRANSLATION
ANTIBODY CROSS REACTION LACTOSE BINDING REVERSAL GALACTOSE BINDING
IMMUNOGLOBULIN E

L5 ANSWER 7 OF 8 MEDLINE on STN

AN 89123243 MEDLINE

DN 89123243 PubMed ID: 2536691

TI Biochemical and immunological comparisons of carbohydrate-binding protein 35 and an IgE-binding protein.

AU Laing J G; Robertson M W; Gritzmacher C A; Wang J L; Liu F T

CS Department of Biochemistry, Michigan State University, East Lansing 48824.

NC AI-19747 (NIAID)

GM-27203 (NIGMS)

GM-38740 (NIGMS)

+

SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1989 Feb 5) 264 (4) 1097-10.

Journal code: 2985121R. ISSN: 0021-9258.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 198903

ED Entered STN: 19900308

Last Updated on STN: 19970203

Entered Medline: 19890313

AB The predicted amino acid sequence of carbohydrate-binding protein 35 (CBP35; Mr approximately 35,000), a galactose-specific lectin in many mouse and human cells, has been compared to the predicted sequence of an IgE-binding protein (epsilon BP) originally identified in rat basophilic leukemia cells. The sequences of the two proteins showed that: (a) 85% of the amino acid residues are identical; (b) the polypeptide chains are comprised of two distinct domains; and (c) highly conserved internal repetitive sequences are present. Consistent with these observations, antisera raised against CBP35 or against a synthetic peptide derived from the epsilon BP sequence cross-reacted with both proteins. Moreover, fractionation of extracts of mouse 3T3 fibroblasts over an IgE-Sepharose affinity column showed that CBP35 bound to IgE; this binding was reversed by addition of lactose. Conversely, fractionation of extracts of rat basophilic leukemia cells over an affinity column of Sepharose derivatized with N-(epsilon-amino-caproyl)-D-galactosamine showed that epsilon BP was a galactose-binding protein. Furthermore, epsilon BP bound to IgE-Sepharose could be eluted by lactose. Finally, transcription and translation in vitro of the cDNA corresponding to epsilon BP yielded a polypeptide containing carbohydrate-binding activity. All of these results strongly support the conclusion that CBP35 and epsilon BP are mouse and rat homologues, respectively.

AB approximately 35,000), a galactose-specific lectin in many mouse and human cells, has been compared to the predicted sequence of an IgE-

binding protein (epsilon BP) originally identified in rat basophilic leukemia cells. The sequences of the two proteins showed that: (a) 85% of the amino acid residues are identical; (b) the polypeptide. . . showed that epsilon BP was a galactose-binding protein. Furthermore, epsilon BP bound to IgE-Sepharose could be eluted by lactose. Finally, **transcription** and **translation** in vitro of the cDNA corresponding to epsilon BP yielded a polypeptide containing carbohydrate-binding activity. All of these results strongly. . .

L5 ANSWER 8 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1982:246218 BIOSIS

DN PREV198274018698; BA74:18698

TI VIRAL GENE PRODUCTS IN ADENOVIRUS TYPE 2 TRANSFORMED HAMSTER CELLS.

AU ESCHER H [Reprint author]

CS INST GENTICS, UNIV COLOGNE, COLOGNE, FEDERAL REPUBLIC OF GERMANY

SO Journal of Virology, (1982) Vol. 41, No. 3, pp. 1076-1082.

CODEN: JOVIAM. ISSN: 0022-538X.

DT Article

FS BA

LA ENGLISH

AB Viral gene products expressed in 5 adenovirus type 2 (Ad2)-transformed hamster embryo cell lines (Ad2 HE1-5) were analyzed by cell-free translation of cytoplasmic, viral RNA which was selected by hybridization to cloned restriction endonuclease fragments of Ad2 DNA. Proteins synthesized in vitro were analyzed by electrophoresis in sodium dodecyl sulfate-polyacrylamide gels and compared with those directed by RNA prepared from productively infected cells. The early regions E1 and E4 of Ad2 were found to be expressed in all of 5 Ad2-transformed hamster embryo cell lines. RNA transcribed from early region E2, which codes for the 72,000-MW (72K) DNA-binding protein was detected in cell line HE1 only, and early region E3 was expressed exclusively in cell line HE4. RNA transcribed from the region .apprx. 12-35 map units, coding for immediate early (13.5K, 52/53K) and intermediate early proteins (13.6K, 16K, 17K, 87K), and RNA from late genes, was not found in any of the cell lines. The proteins synthesized in vitro by RNA prepared from cell lines HE1 to HE5 had electrophoretic mobilities similar to those programmed by RNA from productively infected cells.

AB. . . all of 5 Ad2-transformed hamster embryo cell lines. RNA transcribed from early region E2, which codes for the 72,000-MW (72K) DNA-binding protein was detected in cell line HE1 only, and early region E3 was expressed exclusively in cell line HE4. RNA transcribed from the region .apprx.. . .

IT Miscellaneous Descriptors

EMBRYO CELLS RNA TRANSLATION IMMEDIATE EARLY PROTEINS
TRANSCRIPTION RESTRICTION ENDO NUCLEASE

=>

09/82160

side		result set
<i>DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>		
<u>L13</u>	(detect\$ or identif\$7) near5 (polypeptide\$1 or protein\$1) near5 on (cell\$5 membrane or on cell\$1 or within cell\$1)	0 <u>L13</u>
<u>L12</u>	ELISA near5 (on cell or on cell\$5 membrane)	0 <u>L12</u>
<u>L11</u>	identif\$7 near5 (polypeptide\$1 or protein\$1) near5 (interact\$3 or binid\$3 or contact\$3) near5 (cell\$5 membrane\$1 or on cell\$1 or within cell\$1)	13 <u>L11</u>
<u>L10</u>	l8 and bind\$ moiety and interact\$3	1 <u>L10</u>
<u>L9</u>	L8 and (bind\$3 moiety near5 interact\$3 domain\$1)	0 <u>L9</u>
<u>L8</u>	L7 and (translat\$3 near5 transcrib\$7)	91 <u>L8</u>
<u>L7</u>	L6 and (identif\$7 protein\$1 or identif\$7 polypeptide\$1)	135 <u>L7</u>
<u>L6</u>	(interact\$3 or bind\$3) near5 (cell\$5 membrane or on cell\$1 or within cell\$1)	4167 <u>L6</u>
<u>L5</u>	l4 and (contact\$3 cell\$1 or bind\$3 to cell\$1 or contact\$3 membrane\$1)	0 <u>L5</u>
<u>L4</u>	l3 and ((on or within) cell\$1)	2 <u>L4</u>
<u>L3</u>	L2 and (identif\$7 near5 (polypeptide\$1 or protein\$1) near5 (contact\$3 or bind\$3) near5 (on or within) near5 cell\$1)	2 <u>L3</u>
<u>L2</u>	6265545.pn.	2 <u>L2</u>
<u>L1</u>	6265545.pn	0 <u>L1</u>

END OF SEARCH HISTORY

09/821.160.

```
=> s transcri#####(10a)translat###(10a)polymerase chain reaction#
L1      159 TRANSCRI#####(10A) TRANSLAT###(10A) POLYMERASE CHAIN REACTION#

=> s l1 and (identif#####(10a)(polypeptide# or protein# or peptide#)0
MISSING OPERATOR PEPTIDE#)0
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l1 and (identif#####(10a)(polypeptide# or protein# or peptide#))
L2      13 L1 AND (IDENTIF#####(10A)(POLYPEPTIDE# OR PROTEIN# OR PEPTIDE#
      ))

=>

=> s l2 and bind###
L3      4 L2 AND BIND###

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4      1 DUP REM L3 (3 DUPLICATES REMOVED)

=> d l4 bib ab kwic

L4      ANSWER 1 OF 1      MEDLINE on STN      DUPLICATE 1
AN      90138861      MEDLINE
DN      90138861      PubMed ID: 2153955
TI      DNA amplification-restricted transcription-translation: rapid analysis of
rhesus rotavirus neutralization sites.
CM      Erratum in: Proc Natl Acad Sci U S A 1990 Jun;87(11):4411
AU      Mackow E R; Yamanaka M Y; Dang M N; Greenberg H B
CS      Department of Medicine, Stanford University, CA 94305.
NC      R22 AI1362 (NIAID)
SO      PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
AMERICA, (1990 Jan) 87 (2) 518-22.
Journal code: 7505876. ISSN: 0027-8424.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Priority Journals
EM      199003
ED      Entered STN: 19900328
Last Updated on STN: 19970203
Entered Medline: 19900306
AB      DNA amplification-restricted transcription-translation
(DARTT), is based on DNA amplification by the polymerase
chain reaction (PCR) and uses PCR to truncate
protein-encoding DNA while adding transcriptional and translational
initiation signals to the segment. The amplified DNA segments are
transcribed into RNA and translated into protein in vitro and the
synthesized proteins are used to define functional sites. DARTT was
applied to rhesus rotavirus gene segment 4 cDNA in order to create a
series of carboxyl-terminal truncations and new amino termini in the
encoded VP4 capsid protein. The truncated VP4 polypeptides were tested
for reaction with 11 VP4-specific neutralizing monoclonal antibodies to
identify the minimum polypeptides required for antibody
recognition. Monoclonal antibodies 2G4, M2, and M7, which neutralize a
number of serologically distinct rotaviruses, required amino acids 247-474
of VP4 for binding. DARTT is potentially applicable to the
identification of discontinuous epitopes and functional domains on
a variety of proteins.
AB      DNA amplification-restricted transcription-translation
(DARTT), is based on DNA amplification by the polymerase
chain reaction (PCR) and uses PCR to truncate
protein-encoding DNA while adding transcriptional and translational
```

request a copy 2/12/2004

initiation signals to the segment. The amplified. . . the encoded VP4 capsid protein. The truncated VP4 polypeptides were tested for reaction with 11 VP4-specific neutralizing monoclonal antibodies to identify the minimum polypeptides required for antibody recognition. Monoclonal antibodies 2G4, M2, and M7, which neutralize a number of serologically distinct rotaviruses, required amino acids 247-474 of VP4 for binding. DARTT is potentially applicable to the identification of discontinuous epitopes and functional domains on a variety of proteins.

=> s yu.in.

L5 5753 YU.IN.

=> s l5 and Zhongping

L6 0 L5 AND ZHONGPING